

AMENDMENT

Kindly amend the application, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, as follows.

IN THE SPECIFICATION:

Please amend the specification, without prejudice, without admission, without surrender of subject matter, and without any intention of creating any estoppel as to equivalents, to read as follows:

Please delete the paragraph on page 7, line 14, to page 8, line 2 and replace it with the following paragraph:

Examples of specific primers/probes which target the *cpsD*, *cpsE*, *cpsF*, *cpsG*, *cpsI* or *cpsM* genes include the following **(SEQ ID NOS 1-22, respectively, in order of appearance):**

<i>cpsDS</i>	GCA AAA GAA CAG ATG GAA CAA AGT GG
<i>cpsES</i>	CTT TTG GAG TCG TGG CTA TCT TG
<i>cpsEA1</i>	GA/T/GA AAA AAG GAA AGT CGT GTC G/ATT G
<i>cpsES1</i>	CTT GGA C/TTC CTC TGA AAA GGA TTG
<i>cpsEA2</i>	AAA A/CGC TTG ATC AAC AGT TAA GCA GG
<i>cpsES2</i>	GAT GGT/C GGA CCG GCT ATC TTT TCT C
<i>cpsEA3</i>	CTT AAT TTG TTC TGC ATC TAC TCG C
<i>cpsES3</i>	GTT AGA TGT TCA ATA TAT CAA TGA ATG GTC TAT TTG GTC AG
<i>cpsEFA</i>	CCT TTC AAA CCT TAC CTT TAC TTA GC
<i>cpsFS</i>	CAT CTG GTG CCG CTG TAG CAG TAC CAT T
<i>cpsFA</i>	GTC GAA AAC CTC TAT A/GT A AAC/T GGT CTT ACA A/GCC AAA TAA CTT ACC
<i>cpsGA</i>	AAG/C AGT TCA TAT CAT CAT ATG AGA G
<i>cpsGA1</i>	CCG CCA/G TGT GTG ATA ACA ATC TCA GCT TC
<i>cpsGS</i>	ATG ATG ATA TGA ACT CTT ACA TGA AAG AAG CTG AGA TTG
<i>cpsGS1</i>	GAA CTC TTA CAT GAA AGA AGC TGA GAT TGT TAT CAC AC
<i>IbcpsIA</i>	CTA TCA ATG AAT GAG TCT GTT GTA GGA CGG ATT GCA CG

IbcpsIS GAT AAT AGT GGA GAA ATT TGT GAT AAT TTA TCT CAA AAA GAC G
IbcpsIA1 CCT GAT TCA TTG CAG AAG TCT TTA CGA TGC GAT AGG TG
IVcpsMA GGG TCA ATT GTA TCG TCG CTG TCA ACA AAA CCA ATC AAA TC
VcpsMA CCC CCC ATA AGT ATA AAT AAT ATC CAA TCT TGC ATA GTC AG
VIcpsIA GAA GCA AAG ATT CTA CAC AGT TCT CAA TCA CTA ACT CCG
cpsIA GTA TAA CTT CTA TCA ATG GAT GAG TCT GTT GTA GTA CGG

The primer designations correspond to those given in Table 2.

Please delete the paragraph on page 8, lines 14-33 and replace it with the following paragraph:

Examples of specific primers/probes which target the *alp2*, *alp3* and *rib* genes include the following **(SEQ ID NOS 23-37, respectively, in order of appearance)**:

bcaS1 GGT AAT CTT AAT ATT TTT GAA GAG TCA ATA GTT GCT GCA TCT AC
bcaS2 CCAGGGA GTG CAG CGA CCT TAA ATA CAA GCA TC
balS GAT CCT CAA AAC CTC ATT GTA TTA AAT CCA TCA AGC TAT TC
balA CCA GTT AAG ACT TCA TCA CGA CTC CCA TCA C
bal23S1 CAG ACT GTT AAA GTG GAT GAA GAT ATT ACC TTT ACG G
bal23S2 CTT AAA GCT AAG TAT GAA AAT GAT ATC ATT GGA GCT CGT G
bal2S CTT CCG CCA GAT AAA ATT AAG
bal2A CTG TTG ACT TAT CTG GAT AGG TC
bal2A1 CGT GTT GTT CAA CAG TCC TAT GCT TAG CCT CTG GTG
bal2A2 GGT ATC TGG TTT ATG ACC ATT TTT CCA GTT ATA CG
bal3S GTT CTT CCG CTT AAG GAT AG
bal3A GAC CGT TTG GTC CTT ACC TTT TGG TTC GTT GCT ATC C
ribS2 GAAGTAATTTTCAG GAA GTG CTG TTA CGT TAA ACA CAA ATA TG
ribA1 GAA GGT TGT GTG AAA TAA TTG CCG CCT TGC CTA ATG
ribA2 AAT ACT AGC TGC ACC AAC AGT AGT CAA TTC AGA AGG

The primer designations correspond to those given in Table 6.

Please delete the paragraph on page 9, lines 5-25 and replace it with the following paragraph:

Examples of specific primers/probes which target *IS861*, *IS1548*, *IS1381*, *ISSa4* and *GBSi1* include the following **(SEQ ID NOS 38-55, respectively, in order of appearance)**:

IS861S	GAG AAA ACA AGA GGG AGA CCG AGT AAA ATG GGA CG
IS861A1	CAC GAT TTC GCA GTT CTA AAT AAA TCC GAC GAT AGC C
IS861A2	CAA ACT CCG TCA CAT CGG TAT AGC ACT TCT CAT AGG
IS1548S	CTA TTG ATG ATT GCG CAG TTG AAT TGG ATA GTC GTC
IS1548S1	GTT TGG GAC AGG TAG CGG TTG AGG AGA AAA GTA ATG
IS1548A1	CAT TAC TTT TCT CCT CAA CCG CTA CCT GTC CCA AAC
IS1548A2	CCC AAT ACC ACG TAA CTT ATG CCA TTT G
IS1548A3	CGT GTT ACG AGT CAT CCC AAT ACC ACG TAA CTT ATG CC
IS1381S1	CTT ATG AAC AAA TTG CGG CTG ATT TTG GCA TTC ACG
IS1381S2	GGC TCA GGC GAT TGT CAC AAG CCA AGG GAG
IS1381A	CTA AAA TCC TAG TTC ACG GTT GAT CAT TCC AGC
ISSa4S	CGT ATC TGT CAC TTA TTT CCC TGC GGG TGT CTC C
ISSa4A1	GCC GAT GTC ACA ACA TAG TTC AGG ATA TAG CCA G
ISSa4A2	CGT AAA GGA GTC CAA AGA TGA TAG CCT TTT TGA ACC
GBSi1S1	CAT CTC GGA ACA ATA TGC TCG AAG CTT ACA AGC AAG TG
GBSi1S2	GGG GTC ACT ATC GAG CAG ATG GAT GAC TAT CTT CAC
GBSi1A1	AAT GGC TGT TTC GCA GGA GCG ATT GGG TCT GAA CC
GBSi1A2	CCA GGG ACA TCA ATC TGT CTT GCG GAA CAG TAT CG

Please delete the paragraph on page 15, lines 19-21 and replace it with the following paragraph:

Figure 1. Molecular serotype identification based on the sequence heterogeneity of the 3'-end of *cpsD-cpsE-cpsF*-and the 5'-end of *cpsG* (relevant primers are shown). **The nucleotide sequences are shown in SEQ ID NOS 162-173, respectively, in order of appearance.**

Please delete the paragraph on page 15, lines 26-28 and replace it with the following paragraph:

Figure 3. Multiple sequence alignments of the gene sequences of *cpsG-cpsH-cpsI/M* for serotypes Ia, Ib, II, III, IV, V and VI (start and stop codons are highlighted in bold). **The nucleotide sequences are shown in SEQ ID NOS 174-179, respectively, in order of appearance.**

Please delete the paragraph on page 15, lines 30-32 and replace it with the following paragraph:

Figure 4. Two sites (*) of sequence heterogeneity between alp2 (AF208158, upper lines; **SEQ ID NO: 180**) and alp3 (AF291065, lower lines; **SEQ ID NO: 181**) used to distinguish them (relevant primers are shown).

Please delete the paragraph on page 29, lines 10-20 and replace it with the following paragraph:

Previously, we found a full-length insertion sequence *IS1381* (AF367974) within C beta antigen gene of a clinical isolate, with several differences compared with the original published sequence (AF064785): the terminal inverted repeats contained 15, rather than 20 base pairs (bp); there was a three bp deletion and four individual bp differences in the putative transposase pseudogene between positions 419 to 429 (of the original GenBank sequence) - **GGG ATC CGA TT** (AF064785)(**SEQ ID NO: 182**) vs **CAG A-- -GG TA** (AF367974; our sequence). All amplicons of primer pair IS1381S1/IS1381A from 12 reference and 12 selected clinical isolates were identical with each other and with that of our *IS1381* sequence in GenBank (AF367974) but different, as above, from the original reported *IS1381* sequence (AF064785).

Please delete Table 2 starting on page 45 and replace it with the following table:

Table 2. Oligonucleotide primers used in this study (**SEQ ID NOS 56-115, respectively, in order of appearance.**)

Primer	Target gene	Tm °C ¹	GenBank accession numbers	Sequence ²⁻⁴
CFBS	<i>cfb</i>	56.7	X72754	328GAT GTA TCT ATC TGG AAC TCT AGT G352
Sag59 ⁵	<i>cfb</i>	77.4	X72754	350GTGGCTGGTGCATTGTTAT TTT CAC CAG CTG TAT TAG AAG TA391
Sag190 ⁵	<i>cfb</i>	76.8	X72754	545CATTAAACCGGTTTTTCATAATCT GTT CCC TGA ACA TTA TCT TTG AT500
CFBA	<i>cfb</i>	63.2	X72754	568TTT TTC CAC GCT AGT AAT AGC CTC545
16SS	16S rRNA	69.3	AB023574	1441GCC GCC TAA GGT GGG ATA GAT G1462
23SA	23S rRNA	65.7	X68427	70CGT CGT TTG TCA CGT CCT TC51
DSF2 ⁶	16S rRNA	75.9	AB023574	975CATCCTTCTGACC GGC CTA GAG ATA GGC TTT CT1007
DSR1 ⁶	16S rRNA	81.5	AB023574	1250CGTCACCGG CTT GCG ACT CGT TGT ACC AA1222
cpsDS	<i>cpsD</i>	69.1	AB028896 (Ia), AF163833 (III)	4892/4593GCA AAA GAA CAG ATG GAA CAA AGT GG5007/4618
cpsES	<i>cpsE</i>	65.7	AB028896 (Ia), AF163833 (III)	5300/4910CTT TTG GAG TCG TGG CTA TCT TG5322/4932
cpsEA1	<i>cpsE</i>	65.4	AB028896 (Ia), AF163833 (III)	5431/5041GA/T/GA AAA AAG GAA AGT CGT GTC G/ATT G5612/5017
cpsES1	<i>cpsE</i>	65.9	AB028896 (Ia), AF163833 (III)	5612/5222CTT GGA C/TTC CTC TGA AAA GGA TTG5635/5245
cpsEA2	<i>cpsE</i>	66.8	AB028896 (Ia), AF163833 (III)	5723/5333AAA A/CGC TTG ATC AAC AGT TAA GCA GG5698/5308
cpsES2	<i>cpsE</i>	70.2	AB028896 (Ia), AF163833 (III)	6012/5622GAT GGT/C GGA CCG GCT ATC TTT TCT C6036/5646

cpsEA3	<i>cpsE</i>	63.7	AB028896 (Ia), AF163833 (III)	6116/5726CTT AAT TTG TTC TGC ATC TAC TCG C6092/5702
cpsES3	<i>cpsE</i>	71.5	AB028896 (Ia), AF163833 (III)	6410/6020GTT AGA TGT TCA ATA TAT CAA TGA ATG GTC TAT TTG GTC AG6450/6060
cpsEFA	<i>cpsE/F</i> spacer	62.1	AB028896 (Ia), AF163833 (III)	6526/6136CCT TTC AAA CCT TAC CTT TAC TTA GC6501/6111
cpsFS	<i>cpsF</i>	75.0	AB028896 (Ia), AF163833 (III)	6777/6387CAT CTG GTG CCG CTG TAG CAG TAC CAT T6804/6414
cpsFA	<i>cpsF</i>	73.2	AB028896 (Ia), AF163833 (III)	6859/6469GTC GAA AAC CTC TAT A/GT A AAC/T GGT CTT ACA A/GCC AAA TAA CTT ACC6819/6425
cpsGA	<i>cpsG</i>	54.7	AB028896 (Ia), AF163833 (III)	7162/6772AAG/C AGT TCA TAT CAT CAT ATG AGA G 7138/6748
cpsGA1	<i>cpsG</i>	74.5	AB028896 (Ia), AF163833 (III)	7199/6809CCG CCA/G TGT GTG ATA ACA ATC TCA GCT TC7171/6781
cpsGS	<i>cpsG</i>	72.24	AB028896 (Ia), AF163833 (III)	7145/6755ATG ATG ATA TGA ACT CTT ACA TGA AAG AAG CTG AGA TTG 7183/6793
cpsGS1	<i>cpsG</i>	71.62	AB028896 (Ia), AF163833 (III)	7155/6765GAA CTC TTA CAT GAA AGA AGC TGA GAT TGT TAT CAC AC 7192/6802
IacpsHS	<i>cpsH</i>	73.6	AB028896 (Ia)	7698CAT TCT TTG TTT AAA AA/CT CCT GAT TTT GAT AGA ATT TTA GCA GC7741
IacpsHA	<i>cpsH</i>	75.2	AB028896 (Ia)	7993GAA TAT TCA AAA AAT CCC ATT GCT CTT TGA GTA TGC ATA CC7953
IacpsHA1	<i>cpsH</i>	66.4	AB028896 (Ia)	8271GTA AGT TAT CAA AAT ATA ACA TCA TTA CTA TTA CTA GTA GAA ACG G8226
IacpsHS1	<i>cpsH</i>	77.9	AB028896 (Ia)	8463GGC CTG CTG GGA TTA ATG AAT ATA GTT CCA GGT TTG C8499

IacpsHA2	<i>cpsH</i>	58.5	AB028896 (Ia)	8499 GCA AAC CTG GAA CTA TAT TCA T8478
IbcpsHS0	<i>cpsH</i>	58.6	AB050723 (Ib)	3013 ATT GCT GCA TTC AAT TCA C 3031
IbcpsHS	<i>cpsH</i>	81.9	AB050723 (Ib)	3016 GCT GCA TTC AAT TCA CTG GCA GTA GGG GTT GTG TCC 3051
IbcpsHA	<i>cpsH</i>	67.7	AB050723 (Ib)	3297 GAT AGT TAA GGG TAT TAT AAG ATT TGA ATA TTC AAA GAA AGC 3256
IbcpsHS1	<i>cpsH</i>	74.1	AB050723 (Ib)	3546 TTT GGT GAG CAT ATA TAA TAG AAT AAT CAA TTT GCG GTC G 3585
IbcpsHS2	<i>cpsH</i>	73.7	AB050723 (Ib)	3740 CTG GCC TAT TTG GAC TAA TAA ATG TGA TTT TAG GTT TGT TTC 3781
IbcpsHA01	<i>cpsH</i>	57.7	AB050723 (Ib)	3781 GAA ACA AAC CTA AAA TCA CAT TTA 3758
IbcpsHA1	<i>cpsH</i>	78.5	AB050723 (Ib)	3894 GGC GCC ATC AAT ATC TTC AAG TGC AAA AAA TGA AAA TAG G 3855
IbcpsIA	<i>cpsI</i>	78.2	AB050723 (Ib)	4086 CTA TCA ATG AAT GAG TCT GTT GTA GGA CGG ATT GCA CG 4049
IbcpsIS	<i>cpsI</i>	71.1	AB050723 (Ib)	4116 GAT AAT AGT GGA GAA ATT TGT GAT AAT TTA TCT CAA AAA GAC G 4158
IbcpsIA1	<i>cpsI</i>	78.6	AB050723 (Ib)	4638 CCT GAT TCA TTG CAG AAG TCT TTA CGA TGC GAT AGG TG 4601
IIIVlcpsHS	<i>cpsH</i>	75.3	AF163833 (III), AF337958 (VI)	7275/7120 CAA GAG GAT ATA ACG TTT CAG CGA TTT ATT GCT GAG C 7311/7156
IIlcpsHS	<i>cpsH</i>	72.1	AF163833 (III)	7672 GAA TAC TAT TGG TCT GTA TGT TGG TTT TAT TAG CAT CGC 7710
IIlcpsHA	<i>cpsH</i>	71.0	AF163833 (III)	7817 GTT ATA AGA AAA ACA AGCGGT GAT AAA TAA GAA AGT CAT ACC 7776
IVcpsHS	<i>cpsH</i>	74.1	AF355776 (IV)	7552 CCG TAC ATA CAA CTG TTC TTG TTA GCA TTT ACT TTT CTT TGC 7593
IVcpsHS1	<i>cpsH</i>	71.2	AF355776 (IV)	7887 CCC AAG TAT AGT TAT GAA TAT TAG TTG GAT GGT TTT TGG 7925
IVcpsHA	<i>cpsH</i>	77.3	AF355776 (IV)	7951 CAT CTA CAC CCC CAC AAA ATA TTT TCC CAA AAA CCA TC 7914
IVcpsHA1	<i>cpsH</i>	58.7	AF355776 (IV)	7958 TGT AAA TCA TCT ACA CCC CC 7939
IVcpsMA	<i>cpsM</i>	80.7	AF355776 (IV)	8265 GGG TCA ATT GTA TCG TCG CTG TCA ACA AAA CCA ATC AAA TC 8225
VcpsHS	<i>cpsH</i>	76.3	AF349539 (V)	6943 GGG TTT AGG CGA GGG AAA CTC AGC TTA CAA AAT AGT G 6979

VcpsHS1	<i>cpsH</i>	72.2	AF349539 (V)	7258 CAA TTT TTA TAG GGA TGG ACA ATT TAT TCT GAG AAG TGA C7297
VcpsHA	<i>cpsH</i>	71.1	AF349539 (V)	7291 TCT CAG AAT AAA TTG TCC ATC CCT ATA AAA ATT GAC ATA C7252
VcpsHS02	<i>cpsH</i>	59.0	AF349539 (V)	7616 GAT GTT CTT TTA ACA GGT AGA TTA CAC 7642
VcpsHA1	<i>cpsH</i>	66.8	AF349539 (V)	7658 GTT GTA AAT GAG CAT AGT GTA ATC TAC CTG TTA AAA GAA C7619
VcpsHS2	<i>cpsH</i>	74.0	AF349539 (V)	7871 CCC AGT GTG GTA ATG AAT ATT AGT TGG CTA GTT TTT GG 7908
VcpsHA2	<i>cpsH</i>	58.6	AF349539 (V)	7945 CTT TTT TAT AGG TTC GAT ACC ATC 7922
VcpsMA	<i>cpsM</i>	73.1	AF349539 (V)	8244 CCC CCC ATA AGT ATA AAT AAT ATC CAA TCT TGC ATA GTC AG 8204
VIcpsHS	<i>cpsH</i>	76.7	AF337958 (VI)	7478 CAC TAT TCC TAG TTT TTT GTG CAT ATT TGA CAG GGG CAA G7517
VIcpsHA	<i>cpsH</i>	76.7	AF337958 (VI)	7517 CTT GCC CCT GTC AAA TAT GCA CAA AAA ACT AGG AAT AGT G7478
VIcpsHS1	<i>cpsH</i>	77.2	AF337958 (VI)	7767 CCT TAT TGG GCA AGG TAT AAG AGT TCC CTC CAG TGT G7803
VIcpsHA1	<i>cpsH</i>	77.2	AF337958 (VI)	7804 CCA CAC TGG AGG GAA CTC TTA TAC CTT GCC CAA TAA G7768
VIcpsIA	<i>cpsI</i>	74.5	AF337958 (VI)	8126 GAA GCA AAG ATT CTA CAC AGT TCT CAA TCA CTA ACT CCG 8088
cpsIA	<i>cpsI</i>	70.3	AB028896 (Ia), AF163833 (III)	8816/8312 GTA TAA CTT CTA TCA ATG GAT GAG TCT GTT GTA GTA CGG 8778/8274

Notes.

1. The primer T_m values are provided by the primer synthesiser (Sigma-Aldrich).
2. Numbers represent the numbered base positions at which primer sequences start and finish (numbering start point "1" refer to the start points "1" of correspondent gene GenBank accession numbers).
3. Underlined sequences show bases added to modify previously published primers.
4. Letters behind "/" indicate alternative nucleotides in different serotypes.
5. Ke *et al.*, 2000.
6. Ahmet *et al.*, 1999

Please delete Table 6 starting on page 58 and replace it with the following table:

Table 6. Oligonucleotide primers used in this study (SEQ ID NOS 116-143, respectively, in order of appearance).

Primer	Target gene	T _m °C ¹	GenBank Accession numbers	Sequence ^{2,3}
IgAagGBS ⁵	<i>bac</i>	73.8	X59771	2663 GCGATTAAACAA CAA ACT ATT TTT GAT A TTG ACA ATG CAA 2702
IgAS1 ⁴	<i>bac</i>	72.8	X59771	2765 GCT AAA TTT CAA AAA GGT CTA GAG ACA AAT ACG CCA G 2801
IgAA1 ⁴	<i>bac</i>	78.9	X59771	3157 CCC ATC TGG TAA CTT CGG TGC ATC TGG AAG C 3127
RigAagGBS ⁵	<i>bac</i>	76.3	X59771	3284 CAGCCAACTCTTTC GTC GTT ACT TCC TTG AGA TGT AAC 3247
GBS1360S ⁶	<i>bac</i>	72.3	X59771	1325 GTGAAATTGTAT AAG GCT ATG AGT GAG AGC TTG GAG 1360
GBS1717S ⁴	<i>bac</i>	75.0	X59771	1685 ACA GTC ACA GCT AAA AGT GAT TCG AAG ACG ACG 1717
GBS1937A ⁶	<i>bac</i>	75.9	X59771	1976 CCGTTTTAGAACTCTTT CTG CTC TGG TGT TTT AGG AAC TTG 1937
BcaRUS ⁷	<i>bca</i> repetitive unit	73.5	M97256	769 GATAAATATGATCCAA CAG GAG GGG AAA CAA CAG TAC 805
BcaRUA ⁷	<i>bca</i> repetitive unit	77.2	M97256	1003 CTGGTTTTTGGTGTACAT GAA CCG TTA CTT CTA CTG TAT CC 963
bcaS1 ⁴	<i>bca/alp2/ alp3</i>	71.7	M97256 and AF291065	208/533 GGT AAT CTT AAT ATT TTT GAA GAG TCA ATA GTT GCT GCA TCT AC 251/576
bcaS2 ⁴	<i>bca/alp2/ alp3</i>	78.0	M97256 and AF291065	256/581 CCAGGGA GTG CAG CGA CCT TAA ATA CAA GCA TC 288/613
bcaS ⁴	<i>bca</i>	58.9	M97256	370 GTT TTA GAA CAA GGT TTT ACA GC 392
balS ⁴	<i>alp2/alp3</i>	73.8	AF291065	677 GAT CCT CAA AAC CTC ATT GTA TTA AAT CCA TCA AGC TAT TC 717
bcaA ⁴	<i>bca</i>	74.2	M97256	597 CGTTCTAACTT CTT CAA TCT TAT CCC TCA AGG TTG TTG 560

balA ⁴	<i>alp2/alp3</i>	73.6	AF291065	978 CCA GTT AAG ACT TCA TCA CGA CTC CCA TCA C948
bal23S1 ⁴	<i>alp2/alp3</i>	70.9	AF208158 and AF291065	1093/1373 CAG ACT GTT AAA GTG GAT GAA GAT ATT ACC TTT ACG G1129 /1409
bal23S2 ⁴	<i>alp2/alp3</i>	72.9	AF208158 and AF291065	1174/1454 CTT AAA GCT AAG TAT GAA AAT GAT ATC ATT GGA GCT CGT G1213/1493
bal2S ⁴	<i>alp2</i>	59.2	AF208158	1363 GTT CTT CCG CCA GAT AAA ATT AAG 1386
bal2A ⁴	<i>alp2</i>	58.3	AF208158	1576 CTG TTG ACT TAT CTG GAT AGG TC 1554
bal2A1 ⁴	<i>alp2</i>	78.3	AF208158	1426 CGT GTT GTT CAA CAG TCC TAT GCT TAG CCT CTG GTG 1391
bal2A2 ⁴	<i>alp2</i>	70.8	AF208158	1518 GGT ATC TGG TTT ATG ACC ATT TTT CCA GTT ATA CG 1484
bal3S ⁴	<i>alp3</i>	57.1	AF291065	1643 GTT CTT CCG CTT AAG GAT AGC A 1664
bal3A ⁴	<i>alp3</i>	79.2	AF291065	1693 GAC CGT TTG GTC CTT ACC TTT TGG TTC GTT GCT ATC C 1657
#ribS1 ⁴	<i>rib</i>	65.2	U58333	216 TAC AGA TAC TGT GTT TGC AGC TGA AG 241
ribS2 ⁴	<i>rib</i>	73.0	U58333	238 GAAGTAATTTTCAG GAA GTG CTG TTA CGT TAA ACA CAA ATA TG 279
ribA1 ⁴	<i>rib</i>	78.8	U58333	431 GAA GGT TGT GTG AAA TAA TTG CCG CCT TGC CTA ATG 396
ribA2 ⁴	<i>rib</i>	72.6	U58333	462 AAT ACT AGC TGC ACC AAC AGT AGT CAA TTC AGA AGG 427
#ribA3 ⁴	<i>rib</i>	61.3	U58333	570 CAT CTA TTT TAT CTC TCA AAG CTG AAG 554

Notes.

#For sequencing use only, not entirely specific for rib gene.

1. The primer T_m values are provided by the primer synthesiser (Sigma-Aldrich).
2. Numbers represent the numbered base positions at which primer sequences start and finish (numbering start point "1" refer to the start point "1" of corresponding GenBank accession number, of which there are two for some sequences).
3. Underlined sequences show bases added to modify previously published primers.
4. Primers designed by us for this study.
5. Mawn *et al.*, 1993.

6. Maeland *et al.*, 1997.

7. Maeland *et al.*, 2000.

Please delete Table 10 starting on page 64 and replace it with the following table:

Table 10. Oligonucleotide primers used in this study (**SEQ ID NOS 144-161, respectively, in order of appearance**).

Primer	Target	Tm °C ¹	GenBank accession numbers	Sequence ²
IS861S	IS861	77.4	M22449	445GAG AAA ACA AGA GGG AGA CCG AGT AAA ATG GGA CG479
IS861A1	IS861	77.3	M22449	831CAC GAT TTC GCA GTT CTA AAT AAA TCC GAC GAT AGC C795
IS861A2	IS861	76.1	M22449	1020CAA ACT CCG TCA CAT CGG TAT AGC ACT TCT CAT AGG985
IS1548S	IS1548	76.5	Y14270	143CTA TTG ATG ATT GCG CAG TTG AAT TGG ATA GTC GTC178
IS1548S1	IS1548	77.0	Y14270	539GTT TGG GAC AGG TAG CGG TTG AGG AGA AAA GTA ATG574
IS1548A1	IS1548	77.0	Y14270	574CAT TAC TTT TCT CCT CAA CCG CTA CCT GTC CCA AAC539
IS1548A2	IS1548	70.3	Y14270	915CCC AAT ACC ACG TAA CTT ATG CCA TTT G888
IS1548A3	IS1548	78.0	Y14270	930CGT GTT ACG AGT CAT CCC AAT ACC ACG TAA CTT ATG CC893
IS1381S1	IS1381	80.1	AF064785/ AF367974	272/818CTT ATG AAC AAA TTG CGG CTG ATT TTG GCA TTC ACG307/853
IS1381S2	IS1381	81.7	AF064785/ AF367974	497/1040GGC TCA GGC GAT TGT CAC AAG CCA AGG GAG526/1069

IS1381A	IS1381	73.1	AF064785/ AF367974	881/1424 CTA AAA TCC TAG TTC ACG GTT GAT CAT TCC AGC 849/1392
ISSa4S	ISSa4	78.5	AF165983	326 CGT ATC TGT CAC TTA TTT CCC TGC GGG TGT CTC C359
ISSa4A1	ISSa4	75.2	AF165983	639 GCC GAT GTC ACA ACA TAG TTC AGG ATA TAG CCA G 606
ISSa4A2	ISSa4	74.5	AF165983	780 CGT AAA GGA GTC CAA AGA TGA TAG CCT TTT TGA ACC 745
GBSi1S1	GBSi1	78.6	AJ292930	721 CAT CTC GGA ACA ATA TGC TCG AAG CTT ACA AGC AAG TG 758
GBSi1S2	GBSi1	77.3	AJ292930	789 GGG GTC ACT ATC GAG CAG ATG GAT GAC TAT CTT CAC 824
GBSi1A1	GBSi1	83.9	AJ292930	1058 AAT GGC TGT TTC GCA GGA GCG ATT GGG TCT GAA CC 1024
GBSi1A2	GBSi1	80.5	AJ292930	1161 CCA GGG ACA TCA ATC TGT CTT GCG GAA CAG TAT CG 1127

Notes.

1. The primer Tm values were provided by the primer synthesiser (Sigma-Aldrich).
2. Numbers represent the numbered base positions at which primer sequences start and finish (numbering start point "1" refers to the start point "1" of corresponding gene GenBank accession number).